



DPPIV-5001-C1 PatentIn Replacement Sequence.ST25  
REPLACEMENT SEQUENCE LISTING

<110> Takeda San Diego, Inc.  
<120> CRYSTALLIZATION OF DIPEPTIDYL PEPTIDASE IV (DPPIV)  
<130> DPPIV-5001-C1  
<140> 10/659,055  
<141> 2003-09-09  
<150> US 60/409,206  
<151> 2002-09-09  
<160> 3  
<170> PatentIn version 3.3  
<210> 1  
<211> 766  
<212> PRT  
<213> Homo sapiens  
  
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<221> Amino acid sequence for full-length human wild type DPPIV  
<222> (1)..(766)  
  
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<308> Genbank/NP\_001926  
<309> 2002-02-19  
<313> (1)..(766)  
  
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1 5 10 15  
Leu Val Thr Ile Ile Thr Val Pro Val Val Leu Leu Asn Lys Gly Thr  
20 25 30  
Asp Asp Ala Thr Ala Asp Ser Arg Lys Thr Tyr Thr Leu Thr Asp Tyr  
35 40 45  
Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr Ser Leu Arg Trp Ile Ser  
50 55 60  
Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn Asn Ile Leu Val Phe Asn  
65 70 75 80  
Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu Glu Asn Ser Thr Phe Asp  
85 90 95  
Glu Phe Gly His Ser Ile Asn Asp Tyr Ser Ile Ser Pro Asp Gly Gln  
100 105 110

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Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys Gln Trp Arg His Ser Tyr  
           115                          120                          125  
  
 Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn Lys Arg Gln Leu Ile Thr  
       130                          135                          140  
  
 Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp Val Thr Trp Ser Pro Val  
   145                          150                          155                          160  
  
 Gly His Lys Leu Ala Tyr Val Trp Asn Asn Asp Ile Tyr Val Lys Ile  
                           165                          170                          175  
  
 Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr Trp Thr Gly Lys Glu Asp  
                           180                          185                          190  
  
 Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val Tyr Glu Glu Glu Val Phe  
           195                          200                          205  
  
 Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro Asn Gly Thr Phe Leu Ala  
       210                          215                          220  
  
 Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro Leu Ile Glu Tyr Ser Phe  
   225                          230                          235                          240  
  
 Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys Thr Val Arg Val Pro Tyr  
                           245                          250                          255  
  
 Pro Lys Ala Gly Ala Val Asn Pro Thr Val Lys Phe Phe Val Val Asn  
                           260                          265                          270  
  
 Thr Asp Ser Leu Ser Ser Val Thr Asn Ala Thr Ser Ile Gln Ile Thr  
       275                          280                          285  
  
 Ala Pro Ala Ser Met Leu Ile Gly Asp His Tyr Leu Cys Asp Val Thr  
       290                          295                          300  
  
 Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln Trp Leu Arg Arg Ile Gln  
   305                          310                          315                          320  
  
 Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr Asp Glu Ser Ser Gly Arg  
                           325                          330                          335  
  
 Trp Asn Cys Leu Val Ala Arg Gln His Ile Glu Met Ser Thr Thr Gly  
                           340                          345                          350  
  
 Trp Val Gly Arg Phe Arg Pro Ser Glu Pro His Phe Thr Leu Asp Gly  
           355                          360                          365

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Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu Glu Gly Tyr Arg His Ile  
370 375 380

Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys Thr Phe Ile Thr Lys Gly  
385 390 395 400

Thr Trp Glu Val Ile Gly Ile Glu Ala Leu Thr Ser Asp Tyr Leu Tyr  
405 410 415

Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro Gly Gly Arg Asn Leu Tyr  
420 425 430

Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val Thr Cys Leu Ser Cys Glu  
435 440 445

Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser Val Ser Phe Ser Lys Glu  
450 455 460

Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly Pro Gly Leu Pro Leu Tyr  
465 470 475 480

Thr Leu His Ser Ser Val Asn Asp Lys Gly Leu Arg Val Leu Glu Asp  
485 490 495

Asn Ser Ala Leu Asp Lys Met Leu Gln Asn Val Gln Met Pro Ser Lys  
500 505 510

Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr Lys Phe Trp Tyr Gln Met  
515 520 525

Ile Leu Pro Pro His Phe Asp Lys Ser Lys Lys Tyr Pro Leu Leu Leu  
530 535 540

Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys Ala Asp Thr Val Phe Arg  
545 550 555 560

Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr Glu Asn Ile Ile Val Ala  
565 570 575

Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln Gly Asp Lys Ile Met His  
580 585 590

Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu Val Glu Asp Gln Ile Glu  
595 600 605

Ala Ala Arg Gln Phe Ser Lys Met Gly Phe Val Asp Asn Lys Arg Ile  
610 615 620

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Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr Val Thr Ser Met Val Leu  
625 630 635 640

Gly Ser Gly Ser Gly Val Phe Lys Cys Gly Ile Ala Val Ala Pro Val  
645 650 655

Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr Thr Glu Arg Tyr Met Gly  
660 665 670

Leu Pro Thr Pro Glu Asp Asn Leu Asp His Tyr Arg Asn Ser Thr Val  
675 680 685

Met Ser Arg Ala Glu Asn Phe Lys Gln Val Glu Tyr Leu Leu Ile His  
690 695 700

Gly Thr Ala Asp Asp Asn Val His Phe Gln Gln Ser Ala Gln Ile Ser  
705 710 715 720

Lys Ala Leu Val Asp Val Gly Val Asp Phe Gln Ala Met Trp Tyr Thr  
725 730 735

Asp Glu Asp His Gly Ile Ala Ser Ser Thr Ala His Gln His Ile Tyr  
740 745 750

Thr His Met Ser His Phe Ile Lys Gln Cys Phe Ser Leu Pro  
755 760 765

<210> 2  
<211> 2184  
<212> DNA  
<213> Homo sapiens

<220>  
<221> Human cDNA sequence encoding residues 39-766 of DPPIV  
<222> (1)..(2184)

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ttcaatgctg aatatggaaa cagctcagtt ttcttgagaga acagtacatt tgatgagttt 180  
ggacattcta tcaatgatta ttcaatatct cctgatgggc agtttattct cttagaatac 240  
aactacgtga agcaatggag gcattcctac acagcttcat atgacattta tgatttaa 300  
aaaaggcagc tgattacaga agagaggatt ccaaacaaca cacagtgggt cacatgggtca 360  
ccagtgggtc ataaattggc atatgtttgg aacaatgaca tttatgttaa aattgaacca 420

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|   |      |
|---|------|
| aattttaccaa gttacagaat cacatggacg gggaaagaag atataatata taatggaata  | 480  |
| actgactggg tttatgaaga ggaagtcttc agtgcctact ctgctctgtg gtgggtctcca  | 540  |
| aacggcactt ttttagcata tgcccaattt aacgacacag aagtcccact tattgaatac   | 600  |
| tccttctact ctgatgagtc actgcagtac ccaaagactg tacgggttcc atatccaaag   | 660  |
| gcaggagctg tgaatccaac tgtaaagttc tttgttgtaa atacagactc tctcagctca   | 720  |
| gtcaccaatg caacttccat acaaatact gtcctgctt ctatgttgat aggggatcac     | 780  |
| tacttggtg atgtgacatg ggcaacacaa gaaagaattt ctttgcagtg gctcaggagg    | 840  |
| attcagaact attcgggtcat ggatatttgt gactatgatg aatccagtgg aagatggaac  | 900  |
| tgcttagtgg cacggcaaca cattgaaatg agtactactg gctgggttgg aagatttagg   | 960  |
| ccttcagaac ctcatTTTTac ccttgatggt aatagcttct acaagatcat cagcaatgaa  | 1020 |
| gaagggttaca gacacatttg ctattttccaa atagataaaa aagactgcac atttattaca | 1080 |
| aaaggcacct ggggaagtcat cgggatagaa gctctaacca gtgattatct atactacatt  | 1140 |
| agtaatgaat ataaaggaat gccaggagga aggaatcttt ataaaatcca acttattgac   | 1200 |
| tatacaaaag tgacatgcct cagttgtgag ctgaatccgg aaagggtgtca gtactattct  | 1260 |
| gtgtcattca gtaaagaggc gaagtattat cagctgagat gttccgggtcc tgggtctgccc | 1320 |
| ctctatactc tacacagcag cgtgaatgat aaagggtgta gagtcctgga agacaattca   | 1380 |
| gctttggata aaatgctgca gaatgtccag atgccctcca aaaaactgga cttcattatt   | 1440 |
| ttgaatgaaa caaaattttg gtatcagatg atcttgccctc ctcatTTTga taaatccaag  | 1500 |
| aaatatcctc tactattaga tgtgtatgca ggcccatgta gtcaaaaagc agacactgtc   | 1560 |
| ttcagactga actgggccac ttaccttgca agcacagaaa acattatagt agctagcttt   | 1620 |
| gatggcagag gaagtgggta ccaaggagat aagatcatgc atgcaatcaa cagaagactg   | 1680 |
| ggaacatttg aagttgaaga tcaaattgaa gcagccagac aattttcaaa aatgggattt   | 1740 |
| gtggacaaca aacgaattgc aatttggggc tgggtcatatg gaggggtacgt aacctcaatg | 1800 |
| gtcctgggat cgggaagtgg cgtgttcaag tgtggaatag ccgtggcgcc tgtatccccg   | 1860 |
| tgggagtact atgactcagt gtacacagaa cgttacatgg gtctcccaac tccagaagac   | 1920 |
| aaccttgacc attacagaaa ttcaacagtc atgagcagag ctgaaaattt taaacaagtt   | 1980 |
| gagtacctcc ttattcatgg aacagcagat gataacgttc actttcagca gtcagctcag   | 2040 |
| atctccaaag ccctgggtcga tggtggagtg gatttccagg caatgtggta tactgatgaa  | 2100 |
| gaccatggaa tagctagcag cacagcacac caacatatat ataccacat gagccacttc    | 2160 |
| ataaaacaat gtttctcttt acct  | 2184 |

<210> 3  
<211> 740

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<212> PRT

<213> Homo sapiens

<220>

<221> N-terminal tag including a partial gp67 signal sequence and 6x-histidine

<222> (1)..(12)

<220>

<221> Amino acid sequence for residues 39-766 of DPPIV with an N-terminal tag

<222> (13)..(740)

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Tyr Thr Leu Thr Asp Tyr Leu Lys Asn Thr Tyr Arg Leu Lys Leu Tyr  
20 25 30

Ser Leu Arg Trp Ile Ser Asp His Glu Tyr Leu Tyr Lys Gln Glu Asn  
35 40 45

Asn Ile Leu Val Phe Asn Ala Glu Tyr Gly Asn Ser Ser Val Phe Leu  
50 55 60

Glu Asn Ser Thr Phe Asp Glu Phe Gly His Ser Ile Asn Asp Tyr Ser  
65 70 75 80

Ile Ser Pro Asp Gly Gln Phe Ile Leu Leu Glu Tyr Asn Tyr Val Lys  
85 90 95

Gln Trp Arg His Ser Tyr Thr Ala Ser Tyr Asp Ile Tyr Asp Leu Asn  
100 105 110

Lys Arg Gln Leu Ile Thr Glu Glu Arg Ile Pro Asn Asn Thr Gln Trp  
115 120 125

Val Thr Trp Ser Pro Val Gly His Lys Leu Ala Tyr Val Trp Asn Asn  
130 135 140

Asp Ile Tyr Val Lys Ile Glu Pro Asn Leu Pro Ser Tyr Arg Ile Thr  
145 150 155 160

Trp Thr Gly Lys Glu Asp Ile Ile Tyr Asn Gly Ile Thr Asp Trp Val  
165 170 175

Tyr Glu Glu Glu Val Phe Ser Ala Tyr Ser Ala Leu Trp Trp Ser Pro  
180 185 190

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Asn Gly Thr Phe Leu Ala Tyr Ala Gln Phe Asn Asp Thr Glu Val Pro  
195 200 205

Leu Ile Glu Tyr Ser Phe Tyr Ser Asp Glu Ser Leu Gln Tyr Pro Lys  
210 215 220

Thr Val Arg Val Pro Tyr Pro Lys Ala Gly Ala Val Asn Pro Thr Val  
225 230 235 240

Lys Phe Phe Val Val Asn Thr Asp Ser Leu Ser Ser Val Thr Asn Ala  
245 250 255

Thr Ser Ile Gln Ile Thr Ala Pro Ala Ser Met Leu Ile Gly Asp His  
260 265 270

Tyr Leu Cys Asp Val Thr Trp Ala Thr Gln Glu Arg Ile Ser Leu Gln  
275 280 285

Trp Leu Arg Arg Ile Gln Asn Tyr Ser Val Met Asp Ile Cys Asp Tyr  
290 295 300

Asp Glu Ser Ser Gly Arg Trp Asn Cys Leu Val Ala Arg Gln His Ile  
305 310 315 320

Glu Met Ser Thr Thr Gly Trp Val Gly Arg Phe Arg Pro Ser Glu Pro  
325 330 335

His Phe Thr Leu Asp Gly Asn Ser Phe Tyr Lys Ile Ile Ser Asn Glu  
340 345 350

Glu Gly Tyr Arg His Ile Cys Tyr Phe Gln Ile Asp Lys Lys Asp Cys  
355 360 365

Thr Phe Ile Thr Lys Gly Thr Trp Glu Val Ile Gly Ile Glu Ala Leu  
370 375 380

Thr Ser Asp Tyr Leu Tyr Tyr Ile Ser Asn Glu Tyr Lys Gly Met Pro  
385 390 395 400

Gly Gly Arg Asn Leu Tyr Lys Ile Gln Leu Ser Asp Tyr Thr Lys Val  
405 410 415

Thr Cys Leu Ser Cys Glu Leu Asn Pro Glu Arg Cys Gln Tyr Tyr Ser  
420 425 430

Val Ser Phe Ser Lys Glu Ala Lys Tyr Tyr Gln Leu Arg Cys Ser Gly  
435 440 445

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Pro Gly Leu Pro Leu Tyr Thr Leu His Ser Ser Val Asn Asp Lys Gly  
450 455 460

Leu Arg Val Leu Glu Asp Asn Ser Ala Leu Asp Lys Met Leu Gln Asn  
465 470 475 480

Val Gln Met Pro Ser Lys Lys Leu Asp Phe Ile Ile Leu Asn Glu Thr  
485 490 495

Lys Phe Trp Tyr Gln Met Ile Leu Pro Pro His Phe Asp Lys Ser Lys  
500 505 510

Lys Tyr Pro Leu Leu Leu Asp Val Tyr Ala Gly Pro Cys Ser Gln Lys  
515 520 525

Ala Asp Thr Val Phe Arg Leu Asn Trp Ala Thr Tyr Leu Ala Ser Thr  
530 535 540

Glu Asn Ile Ile Val Ala Ser Phe Asp Gly Arg Gly Ser Gly Tyr Gln  
545 550 555 560

Gly Asp Lys Ile Met His Ala Ile Asn Arg Arg Leu Gly Thr Phe Glu  
565 570 575

Val Glu Asp Gln Ile Glu Ala Ala Arg Gln Phe Ser Lys Met Gly Phe  
580 585 590

Val Asp Asn Lys Arg Ile Ala Ile Trp Gly Trp Ser Tyr Gly Gly Tyr  
595 600 605

Val Thr Ser Met Val Leu Gly Ser Gly Ser Gly Val Phe Lys Cys Gly  
610 615 620

Ile Ala Val Ala Pro Val Ser Arg Trp Glu Tyr Tyr Asp Ser Val Tyr  
625 630 635 640

Thr Glu Arg Tyr Met Gly Leu Pro Thr Pro Glu Asp Asn Leu Asp His  
645 650 655

Tyr Arg Asn Ser Thr Val Met Ser Arg Ala Glu Asn Phe Lys Gln Val  
660 665 670

Glu Tyr Leu Leu Ile His Gly Thr Ala Asp Asp Asn Val His Phe Gln  
675 680 685

Gln Ser Ala Gln Ile Ser Lys Ala Leu Val Asp Val Gly Val Asp Phe  
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690 DPPIV-5001-C1 PatentIn Replacement Sequence.ST25  
695 700

Gln Ala Met Trp Tyr Thr Asp Glu Asp His Gly Ile Ala Ser Ser Thr  
705 710 715 720

Ala His Gln His Ile Tyr Thr His Met Ser His Phe Ile Lys Gln Cys  
725 730 735

Phe Ser Leu Pro  
740